

## SEQUENCE LISTING

## ( 1 ) GENERAL INFORMATION:

( i i i ) NUMBER OF SEQUENCES: 12

## ( 2 ) INFORMATION FOR SEQ ID NO: 1:

## ( i ) SEQUENCE CHARACTERISTICS:

- ( A ) LENGTH: 275 base pairs
- ( B ) TYPE: nucleic acid
- ( C ) STRANDEDNESS: single
- ( D ) TOPOLOGY: linear

( i i ) MOLECULE TYPE: cDNA

## ( v i ) ORIGINAL SOURCE:

- ( A ) ORGANISM: *Aspergillus giganteus*

## ( i x ) FEATURE:

- ( A ) NAME/KEY: 5'UTR
- ( B ) LOCATION: 1..45

## ( i x ) FEATURE:

- ( A ) NAME/KEY: CDS
- ( B ) LOCATION: 46..225
- ( C ) IDENTIFICATION METHOD: experimental
- ( D ) OTHER INFORMATION: /codon\_start= 46
  - / function= "antifungal agent"
  - / product= "antifungal peptide"
  - / evidence= EXPERIMENTAL
  - / note= "antifungal agent, especially on *Rhizoctonia solani*, various *Aspergillus*, *Fusaria* and *Trichophyton* species"

## ( x i ) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

```
TTGCCACCCC CGTTGAAGCC GATTCTCTCA CCGCTGGTGG TCTGG ATG CAA GAG      54
                                     Met Gln Glu
                                     1

ATG AGA GCG CGG GTT TTG GCC ACA TAC AAT GGC AAA TGC TAC AAG AAG      102
Met Arg Ala Arg Val Leu Ala Thr Tyr Asn Gly Lys Cys Tyr Lys Lys
5          10          15

GAT AAT ATC TGC AAG TAC AAG GCA CAG AGC GGC AAG ACT GCC ATT TGC      150
Asp Asn Ile Cys Lys Tyr Lys Ala Gln Ser Gly Lys Thr Ala Ile Cys
20          25          30          35

AAG TGC TAT GTC AAA AAG TGC CCC CGC GAC GGC GCG AAA TGC GAG TTT      198
Lys Cys Tyr Val Lys Lys Cys Pro Arg Asp Gly Ala Lys Cys Glu Phe
40          45          50

GAC AGC TAC AAG GGG AAG TGC TAC TGC TAGACGGTGA GCGAAGGGAC      245
Asp Ser Tyr Lys Gly Lys Cys Tyr Cys
55          60

GAAGTAGGCT GGGGGTTATT TTACTCTGCT      275
```

## ( 2 ) INFORMATION FOR SEQ ID NO: 2:

## ( i ) SEQUENCE CHARACTERISTICS:

- ( A ) LENGTH: 60 amino acids
- ( B ) TYPE: amino acid
- ( D ) TOPOLOGY: linear

( i i ) MOLECULE TYPE: protein

## ( x i ) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

```
Met Gln Glu Met Arg Ala Arg Val Leu Ala Thr Tyr Asn Gly Lys Cys
1          5          10          15

Tyr Lys Lys Asp Asn Ile Cys Lys Tyr Lys Ala Gln Ser Gly Lys Thr
20          25          30
```

5,804,184

11

12

-continued

Ala Ile Cys Lys Cys Tyr Val Lys Lys Cys Pro Arg Asp Gly Ala Lys  
35 40 45  
Cys Glu Phe Asp Ser Tyr Lys Gly Lys Cys Tyr Cys  
50 55 60

## ( 2 ) INFORMATION FOR SEQ ID NO: 3:

## ( i ) SEQUENCE CHARACTERISTICS:

- ( A ) LENGTH: 51 amino acids
- ( B ) TYPE: amino acid
- ( D ) TOPOLOGY: linear

## ( i i ) MOLECULE TYPE: protein

## ( v ) FRAGMENT TYPE: C-terminal

## ( v i ) ORIGINAL SOURCE:

- ( A ) ORGANISM: *Aspergillus giganteus*

## ( i x ) FEATURE:

- ( A ) NAME/KEY: Protein
- ( B ) LOCATION: 1..51
- ( D ) OTHER INFORMATION: /note= "active protein fragment of AFP"

## ( x i ) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

Ala Thr Tyr Asn Gly Lys Cys Tyr Lys Lys Asp Asn Ile Cys Lys Tyr  
1 5 10 15  
Lys Ala Gln Ser Gly Lys Thr Ala Ile Cys Lys Cys Tyr Val Lys Lys  
20 25 30  
Cys Pro Arg Asp Gly Ala Lys Cys Glu Phe Asp Ser Tyr Lys Gly Lys  
35 40 45  
Cys Tyr Cys  
50

## ( 2 ) INFORMATION FOR SEQ ID NO: 4:

## ( i ) SEQUENCE CHARACTERISTICS:

- ( A ) LENGTH: 1032 base pairs
- ( B ) TYPE: nucleic acid
- ( C ) STRANDEDNESS: single
- ( D ) TOPOLOGY: linear

## ( i i ) MOLECULE TYPE: cDNA

## ( v i ) ORIGINAL SOURCE:

- ( A ) ORGANISM: *Hordeum vulgare*
- ( B ) STRAIN: Lcv. Piggy

## ( v i i ) IMMEDIATE SOURCE:

- ( A ) LIBRARY: cDNA gene bank in lambda-gt-11-phages

## ( i x ) FEATURE:

- ( A ) NAME/KEY: 5'UTR
- ( B ) LOCATION: 1..42

## ( i x ) FEATURE:

- ( A ) NAME/KEY: CDS
- ( B ) LOCATION: 43..885
- ( D ) OTHER INFORMATION: /codon\_start= 43
  - / function= "antifungal activity"
  - / product= "protein synthesis inhibitor (PSI)"
  - / note= "antifungal activity, especially on spores of *Trichoderma reesei* and *Fusarium sporotrichoides* and on *Rhizoctonia solani*."

## ( i x ) FEATURE:

- ( A ) NAME/KEY: 3'UTR
- ( B ) LOCATION: 886..1032
- ( D ) OTHER INFORMATION: /partial
  - / note= "46 nucleotides at the 3'-end not shown."

## ( i x ) FEATURE:

-continued

( A ) NAME/KEY: polyA\_signal  
( B ) LOCATION: 930..935  
( D ) OTHER INFORMATION: /note= "potential polyadenylation  
signal"

## ( i x ) FEATURE:

( A ) NAME/KEY: polyA\_signal  
( B ) LOCATION: 963..976  
( D ) OTHER INFORMATION: /note= "potential polyadenylation  
signal"

## ( i x ) FEATURE:

( A ) NAME/KEY: polyA\_signal  
( B ) LOCATION: 1002..1011  
( D ) OTHER INFORMATION: /note= "potential polyadenylation  
signal"

## ( i x ) FEATURE:

( A ) NAME/KEY: mat\_peptide  
( B ) LOCATION: 46..886

## ( x i ) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

CTTAATAGCA CATCTTGTCC GTCTTAGCTT TGCATTACAT CC ATG GCG GCA AAG	54
Met Ala Ala Lys	
1	
ATG GCG AAG AAC GTG GAC AAG CCG CTC TTC ACC GCG ACG TTC AAC GTC	102
Met Ala Lys Asn Val Asp Lys Pro Leu Phe Thr Ala Thr Phe Asn Val	
5 10 15 20	
CAG GCC AGC TCC GCC GAC TAC GCC ACC TTC ATC GCC GGC ATC CGC AAC	150
Gln Ala Ser Ser Ala Asp Tyr Ala Thr Phe Ile Ala Gly Ile Arg Asn	
25 30 35	
AAG CTC CGC AAC CCG GCG CAC TTC TCC CAC AAC CGC CCC GTG CTG CCG	198
Lys Leu Arg Asn Pro Ala His Phe Ser His Asn Arg Pro Val Leu Pro	
40 45 50	
CCG GTC GAG CCC AAC GTC CCG CCG AGC AGG TGG TTC CAC GTC GTG CTC	246
Pro Val Glu Pro Asn Val Pro Pro Ser Arg Trp Phe His Val Val Leu	
55 60 65	
AAG GCC TCG CCG ACC AGC GCC GGG CTC ACG CTG GCC ATT CGG GCG GAC	294
Lys Ala Ser Pro Thr Ser Ala Gly Leu Thr Leu Ala Ile Arg Ala Asp	
70 75 80	
AAC ATC TAC CTG GAG GGC TTC AAG AGC AGC GAC GGC ACC TGG TGG GAG	342
Asn Ile Tyr Leu Glu Gly Phe Lys Ser Ser Asp Gly Thr Trp Trp Glu	
85 90 95 100	
CTC ACC CCG GGC CTC ATC CCC GGC GGC ACC TAC GTC GGG TTC GGC GGC	390
Leu Thr Pro Gly Leu Ile Pro Gly Gly Thr Tyr Val Gly Phe Gly Gly	
105 110 115	
ACC TAC CGC GAC CTC CTC GGC GAC ACC GAC AAG CTG ACC AAC GTC GCT	438
Thr Tyr Arg Asp Leu Leu Gly Asp Thr Asp Lys Leu Thr Asn Val Ala	
120 125 130	
CTC GGC CGG CAG CAG CTC CCG GAC GCG GTG ACC GCC CTC CAC GGG CGC	486
Leu Gly Arg Gln Gln Leu Pro Asp Ala Val Thr Ala Leu His Gly Arg	
135 140 145	
ACC AAG GCC GAC AAG CCG TCC GGC CCG AAG CAG CAG CAG GCG AGG GAG	534
Thr Lys Ala Asp Lys Pro Ser Gly Pro Lys Gln Gln Gln Ala Arg Glu	
150 155 160	
GCG GTG ACG ACG CTG CTC CTC ATG GTG AAC GAG GCC ACG CGG TTC CAG	582
Ala Val Thr Thr Leu Leu Leu Met Val Asn Glu Ala Thr Arg Phe Gln	
165 170 175 180	
ACG GTG TCT GGG TTC GTG GCC GGG TTG CTG CAC CCC AAG GCG GTG GAG	630
Thr Val Ser Gly Phe Val Ala Gly Leu Leu His Pro Lys Ala Val Glu	
185 190 195	
AAG AAG AGC GGG AAG ATC GGC AAT GAG ATG AAG GCC CAG GTG AAC GGG	678
Lys Lys Ser Gly Lys Ile Gly Asn Glu Met Lys Ala Gln Val Asn Gly	
200 205 210	

5,804,184

15

16

-continued

TGG	CAG	GAC	CTG	TCC	GCG	GCG	CTG	CTG	AAG	ACG	GAC	GTG	AAG	CCT	CCG	726
Trp	Gln	Asp	Leu	Ser	Ala	Ala	Leu	Leu	Lys	Thr	Asp	Val	Lys	Pro	Pro	
		215					220					225				
CCG	GGA	AAG	TCG	CCA	GCG	AAG	TTC	GCG	CCG	ATC	GAG	AAG	ATG	GGC	GTG	774
Pro	Gly	Lys	Ser	Pro	Ala	Lys	Phe	Ala	Pro	Ile	Glu	Lys	Met	Gly	Val	
	230					235					240					
AGG	ACG	GCT	GTA	CAG	GCC	GCC	AAC	ACG	CTG	GGG	ATC	CTG	CTG	TTC	GTG	822
Arg	Thr	Ala	Val	Gln	Ala	Ala	Asn	Thr	Leu	Gly	Ile	Leu	Leu	Phe	Val	
245					250					255					260	
GAG	GTG	CCG	GGT	GGG	TTG	ACG	GTG	GCC	AAG	GCG	CTG	GAG	CTG	TTC	CAT	870
Glu	Val	Pro	Gly	Gly	Leu	Thr	Val	Ala	Lys	Ala	Leu	Glu	Leu	Phe	His	
				265					270					275		
GCG	AGT	GGT	GGG	AAA	TAGGTAGTTT	TCCAGGTATA	CCTGCATGGG	TAGTGTAATA								925
Ala	Ser	Gly	Gly	Lys												
			280													
GTCGAATAAA	CATGTCACAG	AGTGACGGAC	TGATATAAAT	AAATAAATAA	ACGTGTCACA											985
GAGTTACATA	TAAACAAATA	AATAAATAAT	TAAAAATGTC	CAGTTTA												1032

( 2 ) INFORMATION FOR SEQ ID NO: 5:

( i ) SEQUENCE CHARACTERISTICS:

( A ) LENGTH: 281 amino acids

( B ) TYPE: amino acid

( D ) TOPOLOGY: linear

( i i ) MOLECULE TYPE: protein

( x i ) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

Met	Ala	Ala	Lys	Met	Ala	Lys	Asn	Val	Asp	Lys	Pro	Leu	Phe	Thr	Ala	
1				5					10					15		
Thr	Phe	Asn	Val	Gln	Ala	Ser	Ser	Ala	Asp	Tyr	Ala	Thr	Phe	Ile	Ala	
			20					25					30			
Gly	Ile	Arg	Asn	Lys	Leu	Arg	Asn	Pro	Ala	His	Phe	Ser	His	Asn	Arg	
		35					40					45				
Pro	Val	Leu	Pro	Pro	Val	Glu	Pro	Asn	Val	Pro	Pro	Ser	Arg	Trp	Phe	
	50					55					60					
His	Val	Val	Leu	Lys	Ala	Ser	Pro	Thr	Ser	Ala	Gly	Leu	Thr	Leu	Ala	
65					70					75					80	
Ile	Arg	Ala	Asp	Asn	Ile	Tyr	Leu	Glu	Gly	Phe	Lys	Ser	Ser	Asp	Gly	
				85					90					95		
Thr	Trp	Trp	Glu	Leu	Thr	Pro	Gly	Leu	Ile	Pro	Gly	[Gly]	Thr	Tyr	Val	
			100					105				Ala	110			
Gly	Phe	Gly	Gly	Thr	Tyr	Arg	Asp	Leu	Leu	Gly	Asp	Thr	Asp	Lys	Leu	
		115					120					125				
Thr	Asn	Val	Ala	Leu	Gly	Arg	Gln	Gln	Leu	[Pro]	Asp	Ala	Val	Thr	Ala	
	130					135				Ala	140					
Leu	His	Gly	Arg	Thr	Lys	Ala	Asp	Lys	Pro	Ser	Gly	Pro	Lys	Gln	Gln	
145					150					155					160	
Gln	Ala	Arg	Glu	Ala	Val	Thr	Thr	Leu	Leu	Leu	Met	Val	Asn	Glu	Ala	
			165					170						175		
Thr	Arg	Phe	Gln	Thr	Val	Ser	Gly	Phe	Val	Ala	Gly	Leu	Leu	His	Pro	
			180					185						190		
Lys	Ala	Val	Glu	Lys	Lys	Ser	Gly	Lys	Ile	Gly	Asn	Gln	Met	Lys	Ala	
		195					200					205				
Gln	Val	Asn	Gly	Trp	Gln	Asp	Leu	Ser	Ala	Ala	Leu	Leu	Lys	Thr	Asp	
	210					215					220					
Val	Lys	Pro	Pro	Pro	Gly	Lys	Ser	Pro	Ala	Lys	Phe	Ala	Pro	Ile	Glu	
225					230					235					240	

-continued

Lys Met Gly Val Arg Thr Ala Val Gln Ala Ala Asn Thr Leu Gly Ile  
245 250 255  
Leu Leu Phe Val Glu Val Pro Gly Gly Leu Thr Val Ala Lys Ala Leu  
260 265 270  
Glu Leu Phe His Ala Ser Gly Gly Lys

## ( 2 ) INFORMATION FOR SEQ ID NO: 6:

## ( i ) SEQUENCE CHARACTERISTICS:

- ( A ) LENGTH: 480 base pairs
- ( B ) TYPE: nucleic acid
- ( C ) STRANDEDNESS: single
- ( D ) TOPOLOGY: linear

## ( i i ) MOLECULE TYPE: cDNA

## ( v i ) ORIGINAL SOURCE:

- ( A ) ORGANISM: Hordeum vulgare
- ( B ) STRAIN: Lcv. Piggy

## ( v i i ) IMMEDIATE SOURCE:

- ( A ) LIBRARY: cDNA gene bank in lambda-gt-11-phages
- ( B ) CLONE: incomplete psi cDNA clone

## ( i x ) FEATURE:

- ( A ) NAME/KEY: CDS
- ( B ) LOCATION: 1..351
- ( D ) OTHER INFORMATION: /partial
  - / codon\_start= 1
  - / function= "protein synthesis inhibitor"
  - / product= "protein synthesis inhibitor"
  - / standard\_name= "PSI"
  - / note= "aminoterminally incomplete protein from an incomplete PSI cDNA clone"

## ( i x ) FEATURE:

- ( A ) NAME/KEY: 3'UTR
- ( B ) LOCATION: 352..487

## ( i x ) FEATURE:

- ( A ) NAME/KEY: polyA\_signal
- ( B ) LOCATION: 404..409
- ( D ) OTHER INFORMATION: /note= "potential polyadenylation signal"

## ( i x ) FEATURE:

- ( A ) NAME/KEY: polyA\_signal
- ( B ) LOCATION: 437..442
- ( D ) OTHER INFORMATION: /note= "potential polyadenylation signal"

## ( i x ) FEATURE:

- ( A ) NAME/KEY: polyA\_signal
- ( B ) LOCATION: 445..450
- ( D ) OTHER INFORMATION: /note= "potential polyadenylation signal"

## ( x i ) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

GCG GTG ACG ACG CTG CTC CTC ATG GTG AAC GAG GCC ACG CGG TTC CAG	48
Ala Val Thr Thr Leu Leu Leu Met Val Asn Glu Ala Thr Arg Phe Gln	
1 5 10 15	
ACG GTG TCG GGG TTC GTG GCC GGG CTG CTG CAC CCC AAG GCG GTG GAG	96
Thr Val Ser Gly Phe Val Ala Gly Leu Leu His Pro Lys Ala Val Glu	
20 25 30	
AAG AAG AGC GGG AAG ATC GGC AAT GAG ATG AAG GCC CAG GTG AAC GGG	144
Lys Lys Ser Gly Lys Ile Gly Asn Glu Met Lys Ala Gln Val Asn Gly	
35 40 45	
TGG CAG GAC CTG TCC GCG GCG CTG CTG AAG ACG GAC GTG AAG CCC CCG	192
Trp Gln Asp Leu Ser Ala Ala Leu Leu Lys Thr Asp Val Lys Pro Pro	
50 55 60	

5,804,184

19

20

-continued

CCG	GGA	AAG	TCG	CCA	GCG	AAG	TTC	ACG	CCG	ATC	GAG	AAG	ATG	GGC	GTG	240
Pro	Gly	Lys	Ser	Pro	Ala	Lys	Phe	Thr	Pro	Ile	Glu	Lys	Met	Gly	Val	
65					70				75						80	
AGG	ACT	GCT	GAG	CAG	GCT	GCG	GCT	ACT	TTG	GGG	ATC	CTG	CTG	TTC	GTT	288
Arg	Thr	Ala	Glu	Gln	Ala	Ala	Ala	Thr	Leu	Gly	Ile	Leu	Leu	Phe	Val	
				85					90						95	
GAG	GTG	CCG	GGT	GGG	TTG	ACG	GTG	GCC	AAG	GCG	CTG	GAG	CTG	TTT	CAT	336
Glu	Val	Pro	Gly	Gly	Leu	Thr	Val	Ala	Lys	Ala	Leu	Glu	Leu	Phe	His	
			100					105						110		
GCG	AGT	GGT	GGG	AAA	TAGGTAGTTT	TGCAGGTATA	CCTGCATGGG	TAAATGTAAA								391
Ala	Ser	Gly	Gly	Lys												
			115													
AGTCGAATAA	AAATGTCACA	GAGTGACGGA	CTGATATAAA	TAAATTAATA	AACATGTCAT											451
CATGAGTGAC	AGACTGATAT	AAATAAATA														480

## ( 2 ) INFORMATION FOR SEQ ID NO: 7:

## ( i ) SEQUENCE CHARACTERISTICS:

- ( A ) LENGTH: 117 amino acids
- ( B ) TYPE: amino acid
- ( D ) TOPOLOGY: linear

## ( i i ) MOLECULE TYPE: protein

## ( x i ) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

Ala	Val	Thr	Thr	Leu	Leu	Leu	Met	Val	Asn	Glu	Ala	Thr	Arg	Phe	Gln	
1				5					10					15		
Thr	Val	Ser	Gly	Phe	Val	Ala	Gly	Leu	Leu	His	Pro	Lys	Ala	Val	Glu	
			20					25					30			
Lys	Lys	Ser	Gly	Lys	Ile	Gly	Asn	Glu	Met	Lys	Ala	Gln	Val	Asn	Gly	
			35				40					45				
Trp	Gln	Asp	Leu	Ser	Ala	Ala	Leu	Leu	Lys	Thr	Asp	Val	Lys	Pro	Pro	
	50					55					60					
Pro	Gly	Lys	Ser	Pro	Ala	Lys	Phe	Thr	Pro	Ile	Glu	Lys	Met	Gly	Val	
65					70					75					80	
Arg	Thr	Ala	Glu	Gln	Ala	Ala	Ala	Thr	Leu	Gly	Ile	Leu	Leu	Phe	Val	
				85					90						95	
Glu	Val	Pro	Gly	Gly	Leu	Thr	Val	Ala	Lys	Ala	Leu	Glu	Leu	Phe	His	
			100					105						110		
Ala	Ser	Gly	Gly	Lys												
			115													

## ( 2 ) INFORMATION FOR SEQ ID NO: 8:

## ( i ) SEQUENCE CHARACTERISTICS:

- ( A ) LENGTH: 2329 base pairs
- ( B ) TYPE: nucleic acid
- ( C ) STRANDEDNESS: single
- ( D ) TOPOLOGY: linear

## ( i i ) MOLECULE TYPE: cDNA

## ( v i ) ORIGINAL SOURCE:

- ( A ) ORGANISM: *Serratia marcescens*

## ( v i i ) IMMEDIATE SOURCE:

- ( A ) LIBRARY: Cosmid bank from *Serratia marcescens*

## ( i x ) FEATURE:

- ( A ) NAME/KEY: misc\_feature
- ( B ) LOCATION: 1..2329
- ( C ) IDENTIFICATION METHOD: experimental
- ( D ) OTHER INFORMATION: /function="exo-chitinase"  
/ product= "ChiS protein"  
/ evidence= EXPERIMENTAL

-continued

/ note= "sequence listing of the ChiS gene from a  
plasmid pLChiS from E.coli A 5187"

( x i ) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

CAGGGCGTTG	TCAATAATGA	CAACACCCTG	GCTGAAGAGT	GTGGTGCAAT	ACTGATAAAT	60
ATTTATCTTT	CCTTAATAGA	AAATTCACCTA	TCCTTATTTG	TCATGTTTTTC	TTTTATTTAT	120
ATGAAAATAA	ATTCACGCTT	GCTGAATAAA	ACCCAGTTGA	TAGCGCTCTT	GTTTTTGCGC	180
CTTTTTTATT	TATAGTACTG	AATGTACGCG	GTGGGAATGA	TTATTTTCGCC	ACGTGGAAAG	240
ACGCTGTTGT	TATTTATTGA	TTTTAACCTT	CGCGGATTAT	TGCGGAATTT	TTTCGCTTCG	300
GCAATGCATC	GCGACGATTA	ACTCTTTTAT	GTTTATCCTC	TCGGAATAAA	GGAATCAGTT	360
ATGCGCAAAT	TTAATAAACC	GCTGTTGGCG	CTGTTGATCG	GCAGCACGCT	GTGTTCCGCG	420
GCGCAGGCCG	CCGCGCCGGG	CAAGCCGACC	ATCGCCTGGG	GCAACACCAA	GTTCCGCCATC	480
GTTGAAGTTG	ACCAGGCGGC	TACCGCTTAT	AATAATTTGG	TGAAGGTAAA	AAATGCCGCC	540
GATGTTTCCG	TCTCCTGGAA	TTTATGGAAT	GGCGACACCG	GCACGACGGC	AAAAGTTTTA	600
TTAAATGGCA	AAGAGGCGTG	GAGTGGTCCT	TCAACCGGAT	CTTCCGGTAC	GGCGAATTTT	660
AAAGTGAATA	AAGGCGGCCG	TTATCAAATG	CAGGTGGCAC	TGTGCAATGC	CGACGGCTGC	720
ACCGCCAGTG	ACGCCACCGA	AATTGTGGTA	GCCGACACCG	ACGGCAGCCA	TTTGGCGCCG	780
TTGAAAGAGC	CGCTGCTGGA	AAAGAATAAA	CCGTATAAAC	AGAACTCCGG	CAAAGTGGTC	840
GGTTCTTATT	TCGTCGAGTG	GGGCGTTTAC	GGGCGCAATT	TCACCGTCGA	CAAGATCCCG	900
GCGCAAAACC	TGACCCACCT	GCTGTACGGC	TTTATCCCGA	TCTGCGGCGG	CAATGGCATC	960
AACGACAGCC	TGAAAGAGAT	TGAAGGCAGC	TTCCAGGCGT	TGCAGCGCTC	CTGCCAGGGC	1020
CGCGAGGACT	TCAAAGTCTC	GATCCACGAT	CCGTTTCGCCC	CGCTGCAAAA	AGCGCAGAAG	1080
GGCGTGACCG	CCTGGGATGA	CCCCTACAAG	GGCAACTTCG	GCCAGCTGAT	GGCGCTGAAG	1140
CAGGCGCATC	CTGACCTGAA	AATCCTGCCG	TCGATCGGCG	GCTGGACGCT	GTCCGACCCG	1200
TTCTTCTTCA	TGGGCGACAA	GGTGAAGCGC	GATCGCTTCG	TCGGTTCGGT	GAAAGAGTTC	1260
CTGCAGACCT	GGAAGTTCTT	CGACGGCGTG	GATATCGACT	GGGAGTTCCC	GGGCGGCAAA	1320
GGCGCCAACC	CTAACCTGGG	CAGCCCGCAA	GACGGGGAAA	CCTATGTGCT	GCTGATGAAG	1380
GAGCTGCGGG	CGATGCTGGA	TCAGCTGTCT	GTGGAAACCG	GCCGCAAGTA	TGAGCTGACC	1440
TCCGCCATCA	GCGCCGGTAA	GGACAAGATC	GACAAGGTGG	CTTACAACGT	TGCGCAGAAC	1500
TCGATGGATC	ACATCTTCCT	GATGAGCTAC	GACTTCTATG	GCGCCTTCGA	TCTGAAGAAC	1560
CTGGGGCATC	AGACCGCGCT	GAATGCGCCG	GCCTGGAAAC	CGGACACCGC	CTACACCACG	1620
GTGAACGGCG	TCAATGCGCT	GCTGGCGCAG	GGCGTCAAGC	CGGGCAAAAT	CGTCGTCCGC	1680
ACCGCCATGT	ATGGCCGCGG	CTGGACCGGG	GTGAACGGCT	ACCAGAACAA	TATTCCGTTC	1740
ACCGGCACCG	CCACCGGGCC	GGTTAAAGGC	ACCTGGGAGA	ACGGTATCGT	GGACTACCGC	1800
CAAATCGCCG	GCCAGTTCAT	GAGCGGCGAG	TGGCAGTATA	CCTACGACGC	CACGGCGGAA	1860
GCGCCTTACG	TGTTCAAACC	TTCCACCGGC	GATCTGATCA	CCTTCGACGA	TGCCCGCTCG	1920
GTGCAGGCTA	AAGGCAAGTA	CGTGTTGGAT	AAGCAGCTGG	GCGGCCTGTT	CTCCTGGGAG	1980
ATCGACGCGG	ATAACGGCGA	TATTCTCAAC	AGCATGAACG	CCAGCCTGGG	CAACAGCGCC	2040
GGCGTTCAAT	AATCGGTTGC	AGTGGTTGCC	GGGGGATATC	CTTTCGCCCC	CGGCTTTTTTC	2100
GCCGACGAAA	GTTTTTTTAC	GCCGCACAGA	TTGTGGCTCT	GCCCCGAGCA	AAACGCGCTC	2160
ATCGGACTCA	CCCTTTTGGG	TAATCCTTCA	GCATTTCTCT	CTGTCTTTAA	CGGCGATCAC	2220
AAAAATAACC	GTTCAGATAT	TCATCATTCA	GCAACAAAGT	TTTGGCGTTT	TTTAACGGAG	2280

-continued

TTAAAAACCA GTAAGTTTGT GAGGGTCAGA CCAATGCGCT AAAAATGGG

2329

## ( 2 ) INFORMATION FOR SEQ ID NO: 9:

## ( i ) SEQUENCE CHARACTERISTICS:

- ( A ) LENGTH: 1002 base pairs
- ( B ) TYPE: nucleic acid
- ( C ) STRANDEDNESS: single
- ( D ) TOPOLOGY: linear

## ( i i ) MOLECULE TYPE: cDNA

## ( v i ) ORIGINAL SOURCE:

- ( A ) ORGANISM: *Hordeum vulgare*
- ( B ) STRAIN: L

## ( i x ) FEATURE:

- ( A ) NAME/KEY: 5'UTR
- ( B ) LOCATION: 1..63

## ( i x ) FEATURE:

- ( A ) NAME/KEY: CDS
- ( B ) LOCATION: 64..861
- ( D ) OTHER INFORMATION: /codon\_start= 64  
/ function= "chitinase"  
/ product= "26 kD preprotein of chitinase G (ChiG)"  
/ note= "antifungal activity, especially on  
*Trichoderma reesei* and *Fusarium sporotrichoides* as  
well as *Rhizoctonia solani* and *Botrytis cinerea*."

## ( i x ) FEATURE:

- ( A ) NAME/KEY: 3'UTR
- ( B ) LOCATION: 862..1002
- ( D ) OTHER INFORMATION: /partial  
/ note= "11 nucleotides at 3'end not shown"

## ( i x ) FEATURE:

- ( A ) NAME/KEY: polyA\_signal
- ( B ) LOCATION: 905..910
- ( D ) OTHER INFORMATION: /note= "potential polyadenylation  
signal"

## ( i x ) FEATURE:

- ( A ) NAME/KEY: sig\_peptide
- ( B ) LOCATION: 64..294
- ( D ) OTHER INFORMATION: /note= "probable signal peptide  
sequence"

## ( i x ) FEATURE:

- ( A ) NAME/KEY: sig\_peptide
- ( B ) LOCATION: 298..312
- ( D ) OTHER INFORMATION: /note= "probable signal peptide  
sequence"

## ( i x ) FEATURE:

- ( A ) NAME/KEY: sig\_peptide
- ( B ) LOCATION: 349..378
- ( D ) OTHER INFORMATION: /note= "probable signal peptide  
sequence"

## ( i x ) FEATURE:

- ( A ) NAME/KEY: sig\_peptide
- ( B ) LOCATION: 466..588
- ( D ) OTHER INFORMATION: /note= "probable signal peptide  
sequence"

## ( i x ) FEATURE:

- ( A ) NAME/KEY: sig\_peptide
- ( B ) LOCATION: 607..861
- ( D ) OTHER INFORMATION: /note= "probable signal peptide  
sequence"

## ( i x ) FEATURE:

- ( A ) NAME/KEY: mat\_peptide
- ( B ) LOCATION: 133..861

## ( x i ) SEQUENCE DESCRIPTION: SEQ ID NO: 9:



5,804,184

25

26

-continued

CCTACGACAG TAGCGTAACG GTAAACACCG AGTACGGTAC TCTGTGCTTT GTTGGCTCGC																60					
ACA	ATG	AGA	TCG	CTC	GCG	GTG	GTG	GTG	GCC	GTG	GTA	GCC	ACG	GTG	GCC	108					
	Met	Arg	Ser	Leu	Ala	Val	Val	Val	Ala	Val	Val	Ala	Thr	Val	Ala						
	-23			-20					-15					-10							
ATG	GCC	ATC	GGC	ACG	GCG	CGC	GGC	AGC	GTG	TCC	TCC	ATC	GTC	TCG	CGC	156					
Met	Ala	Ile	Gly	Thr	Ala	Arg	Gly	Ser	Val	Ser	Ser	Ile	Val	Ser	Arg						
			-5					1				5									
GCA	CAG	TTT	GAC	CGC	ATG	CTT	CTC	CAC	CGC	AAC	GAC	GGC	GCC	TGC	CAG	204					
Ala	Gln	Phe	Asp	Arg	Met	Leu	Leu	His	Arg	Asn	Asp	Gly	Ala	Cys	Gln						
	10					15					20										
GCC	AAG	GGC	TTC	TAC	ACC	TAC	GAC	GCC	TTC	GTC	GCC	GCC	GCA	GCC	GCC	252					
Ala	Lys	Gly	Phe	Tyr	Thr	Tyr	Asp	Ala	Phe	Val	Ala	Ala	Ala	Ala	Ala						
25					30					35					40						
TTC	CCG	GGC	TTC	GGC	ACC	ACC	GGC	AGC	GCC	GAC	GCC	CAG	AAG	CGC	GAG	300					
Phe	Pro	Gly	Phe	Gly	Thr	Thr	Gly	Ser	Ala	Asp	Ala	Gln	Lys	Arg	Glu						
				45					50					55							
GTG	GCC	GCC	TTC	CTA	GCA	CAG	ACC	TCC	CAC	GAG	ACC	ACC	GGC	GGG	TGG	348					
Val	Ala	Ala	Phe	Leu	Ala	Gln	Thr	Ser	His	Glu	Thr	Thr	Gly	Gly	Trp						
			60					65					70								
GCG	ACT	GCA	CCG	GAC	GGG	GCC	TTC	GCC	TGG	GGC	TAC	TGC	TTC	AAG	CAG	396					
Ala	Thr	Ala	Pro	Asp	Gly	Ala	Phe	Ala	Trp	Gly	Tyr	Cys	Phe	Lys	Gln						
		75					80					85									
GAA	CGT	GGC	GCC	TCC	TCC	GAC	TAC	TGC	ACC	CCG	AGC	GCA	CAA	TGG	CCG	444					
Glu	Arg	Gly	Ala	Ser	Ser	Asp	Tyr	Cys	Thr	Pro	Ser	Ala	Glu	Trp	Pro						
	90					95					100										
TGC	GCC	CCC	GGG	AAG	CGC	TAC	TAC	GGC	CGC	GGG	CCA	ATC	CAG	CTC	TCC	492					
Cys	Ala	Pro	Gly	Lys	Arg	Tyr	Tyr	Gly	Arg	Gly	Pro	Ile	Gln	Leu	Ser						
105					110					115					120						
CAC	AAC	TAC	AAC	TAT	GGA	CCT	GCC	GGC	CGG	GCC	ATC	GGG	GTC	GAT	CTG	540					
His	Asn	Tyr	Asn	Tyr	Gly	Pro	Ala	Gly	Arg	Ala	Ile	Gly	Val	Asp	Leu						
				125					130					135							
CTG	GCC	AAC	CCG	GAC	CTG	GTG	GCC	ACG	GAC	GCC	ACT	GTG	GGC	TTT	AAG	588					
Leu	Ala	Asn	Pro	Asp	Leu	Val	Ala	Thr	Asp	Ala	Thr	Val	Gly	Phe	Lys						
			140					145					150								
ACG	GCC	ATC	TGG	TTC	TGG	ATG	ACG	GCG	CAG	CCG	CCC	AAG	CCA	TCG	AGC	636					
Thr	Ala	Ile	Trp	Phe	Trp	Met	Thr	Ala	Gln	Pro	Pro	Lys	Pro	Ser	Ser						
		155					160					165									
CAT	GCT	GTG	ATC	GCC	GGC	CAG	TGG	AGC	CCG	TCA	GGG	GCT	GAC	CGG	GCC	684					
His	Ala	Val	Ile	Ala	Gly	Gln	Trp	Ser	Pro	Ser	Gly	Ala	Asp	Arg	Ala						
	170					175					180										
GCA	GGC	CGG	GTG	CCC	GGG	TTT	GGT	GTG	ATC	ACC	AAC	ATC	ATC	AAC	GGC	732					
Ala	Gly	Arg	Val	Pro	Gly	Phe	Gly	Val	Ile	Thr	Asn	Ile	Ile	Asn	Gly						
185					190					195					200						
GGG	ATC	GAG	TGC	GGT	CAC	GGG	CAG	GAC	AGC	CGC	GTC	GCC	GAT	CGA	ATC	780					
Gly	Ile	Glu	Cys	Gly	His	Gly	Gln	Asp	Ser	Arg	Val	Ala	Asp	Arg	Ile						
			205					210						215							
GGG	TTT	TAC	AAG	CGC	TAC	TGT	GAC	ATC	CTC	GGC	GTT	GGC	TAC	GGC	AAC	828					
Gly	Phe	Tyr	Lys	Arg	Tyr	Cys	Asp	Ile	Leu	Gly	Val	Gly	Tyr	Gly	Asn						
			220					225					230								
AAC	CTC	GAT	TGC	TAC	AGC	CAG	AGA	CCC	TTC	GCC	TAATTAATTA GTCATGTATT					881					
Asn	Leu	Asp	Cys	Tyr	Ser	Gln	Arg	Pro	Phe	Ala											
		235					240														
AATCTTGGCC CTCCATAAAA TACAATAAGA GCATCGTCTC CTATCTACAT GCTGTAAGAT																941					
GTAACATATGG TAACCTTTTA TGGGGAACAT AACAAAGGCA TCTCGTATAG ATGCTTTGCT																1001					
A																1002					

( 2 ) INFORMATION FOR SEQ ID NO:10:

( 1 ) SEQUENCE CHARACTERISTICS:

-continued

( A ) LENGTH: 266 amino acids  
( B ) TYPE: amino acid  
( D ) TOPOLOGY: linear

( i i ) MOLECULE TYPE: protein

( x i ) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Met - 23	Arg	Ser	Leu - 20	Ala	Val	Val	Val	Ala - 15	Val	Val	Ala	Thr	Val - 10	Ala	Met
Ala	Ile	Gly - 5	Thr	Ala	Arg	Gly	Ser 1	Val	Ser	Ser	Ile 5	Val	Ser	Arg	Ala
Gln 10	Phe	Asp	Arg	Met	Leu 15	Leu	His	Arg	Asn	Asp 20	Gly	Ala	Cys	Gln	Ala 25
Lys	Gly	Phe	Tyr	Thr 30	Tyr	Asp	Ala	Phe	Val 35	Ala	Ala	Ala	Ala	Ala 40	Phe
Pro	Gly	Phe	Gly 45	Thr	Thr	Gly	Ser	Ala 50	Asp	Ala	Gln	Lys	Arg 55	Glu	Val
Ala	Ala	Phe 60	Leu	Ala	Gln	Thr	Ser 65	His	Glu	Thr	Thr	Gly 70	Gly	Trp	Ala
Thr	Ala 75	Pro	Asp	Gly	Ala	Phe 80	Ala	Trp	Gly	Tyr	Cys 85	Phe	Lys	Gln	Glu
Arg 90	Gly	Ala	Ser	Ser	Asp 95	Tyr	Cys	Thr	Pro	Ser 100	Ala	Gln	Trp	Pro	Cys 105
Ala	Pro	Gly	Lys	Arg 110	Tyr	Tyr	Gly	Arg	Gly 115	Pro	Ile	Gln	Leu	Ser 120	His
Asn	Tyr	Asn	Tyr 125	Gly	Pro	Ala	Gly	Arg 130	Ala	Ile	Gly	Val	Asp 135	Leu	Leu
Ala	Asn 140	Pro	Asp	Leu	Val	Ala	Thr 145	Asp	Ala	Thr	Val	Gly 150	Phe	Lys	Thr
Ala 155	Ile	Trp	Phe	Trp	Met	Thr 160	Ala	Gln	Pro	Pro	Lys 165	Pro	Ser	Ser	His
Ala 170	Val	Ile	Ala	Gly	Gln 175	Trp	Ser	Pro	Ser	Gly 180	Ala	Asp	Arg	Ala	Ala 185
Gly	Arg	Val	Pro	Gly 190	Phe	Gly	Val	Ile	Thr 195	Asn	Ile	Ile	Asn	Gly 200	Gly
Ile	Glu	Cys	Gly 205	His	Gly	Gln	Asp	Ser 210	Arg	Val	Ala	Asp	Arg 215	Ile	Gly
Phe	Tyr	Lys 220	Arg	Tyr	Cys	Asp	Ile 225	Leu	Gly	Val	Gly	Tyr 230	Gly	Asn	Asn
Leu 235	Asp	Cys	Tyr	Ser	Gln	Arg 240	Pro	Phe	Ala						

( 2 ) INFORMATION FOR SEQ ID NO:11:

( i ) SEQUENCE CHARACTERISTICS:

- ( A ) LENGTH: 1235 base pairs
- ( B ) TYPE: nucleic acid
- ( C ) STRANDEDNESS: single
- ( D ) TOPOLOGY: linear

( i i ) MOLECULE TYPE: cDNA

( v i ) ORIGINAL SOURCE:

( A ) ORGANISM: *Hordeum vulgare*  
( B ) STRAIN: L.

( i x ) FEATURE:

( A ) NAME/KEY: 5'UTR  
( B ) LOCATION: 1..48

( i x ) FEATURE:

( A ) NAME/KEY: CDS

5,804,184

29

30

-continued

( B ) LOCATION: 49..1050  
 ( D ) OTHER INFORMATION: /partial  
     / codon\_start= 49  
     / function= "glucanase"  
     / product= "preprotein of the glucanase GluG"

( i x ) FEATURE:  
     ( A ) NAME/KEY: 3'UTR  
     ( B ) LOCATION: 1051..1235  
     ( D ) OTHER INFORMATION: /partial  
         / note= "14 nucleotides at the 3'end not shown."

( i x ) FEATURE:  
     ( A ) NAME/KEY: polyA\_signal  
     ( B ) LOCATION: 1083..1088  
     ( D ) OTHER INFORMATION: /note= "potential polyadenylation  
         signal"

( i x ) FEATURE:  
     ( A ) NAME/KEY: polyA\_signal  
     ( B ) LOCATION: 1210..1215  
     ( D ) OTHER INFORMATION: /note= "potential polyadenylation  
         signal"

( i x ) FEATURE:  
     ( A ) NAME/KEY: mat\_peptide  
     ( B ) LOCATION: 133..1050

( x i ) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

GGCAGCATTG CATAGCATTT GAGCACCAGA TACTCCGTGT GTGCACCA ATG GCT AGA	57
Met Ala Arg	
- 28	
AAA GAT GTT GCC TCC ATG TTT GCA GTT GCT CTC TTC ATT GGA GCA TTC	105
Lys Asp Val Ala Ser Met Phe Ala Val Ala Leu Phe Ile Gly Ala Phe	
- 25 - 20 - 15 - 10	
GCT GCT GTT CCT ACG AGT GTG CAG TCC ATC GGC GTA TGC TAC GGC GTG	153
Ala Ala Val Pro Thr Ser Val Gln Ser Ile Gly Val Cys Tyr Gly Val	
- 5 1 5	
ATC GGC AAC AAC CTC CCC TCC CGG AGC GAC GTG GTG CAG CTC TAC AGG	201
Ile Gly Asn Asn Leu Pro Ser Arg Ser Asp Val Val Gln Leu Tyr Arg	
10 15 20	
TCC AAG GGC ATC AAC GGC ATG CGC ATC TAC TTC GCC GAC GGG CAG GCC	249
Ser Lys Gly Ile Asn Gly Met Arg Ile Tyr Phe Ala Asp Gly Gln Ala	
25 30 35	
CTC TCG GCC GTC CGC AAC TCC GGC ATC GGC CTC ATC CTC GAC ATC GGC	297
Leu Ser Ala Val Arg Asn Ser Gly Ile Gly Leu Ile Leu Asp Ile Gly	
40 45 50 55	
AAC GAC CAG CTC GCC AAC ATC GCC GCC AGC ACC TCC AAC GCG GCC TCC	345
Asn Asp Gln Leu Ala Asn Ile Ala Ala Ser Thr Ser Asn Ala Ala Ser	
60 65 70	
TGG GTC CAG AAC AAC GTG CGG CCC TAC TAC CCT GCC GTG AAC ATC AAG	393
Trp Val Gln Asn Asn Val Arg Pro Tyr Tyr Pro Ala Val Asn Ile Lys	
75 80 85	
TAC ATC GCC GCC GGC AAC GAG GTG CAG GGC GGC GCC ACG CAG AGC ATC	441
Tyr Ile Ala Ala Gly Asn Glu Val Gln Gly Gly Ala Thr Gln Ser Ile	
90 95 100	
CTG CCG GCC ATG CGC AAC CTC AAC GCG GCC CTC TCC GCG GCG GGG CTC	489
Leu Pro Ala Met Arg Asn Leu Asn Ala Ala Leu Ser Ala Ala Gly Leu	
105 110 115	
GGC GCC ATC AAG GTG TCC ACC TCC ATC CGG TTC GAC GAG GTG GCC AAC	537
Gly Ala Ile Lys Val Ser Thr Ser Ile Arg Phe Asp Glu Val Ala Asn	
120 125 130 135	
TCC TTC CCG CCC TCC GCC GGC GTG TTC AAG AAC GCC TAC ATG ACG GAC	585
Ser Phe Pro Pro Ser Ala Gly Val Phe Lys Asn Ala Tyr Met Thr Asp	
140 145 150	

**-continued**

[illegible]

( 2 ) INFORMATION FOR SEQ ID NO: 12:

( i ) SEQUENCE CHARACTERISTICS:

- ( A ) LENGTH: 334 amino acids  
( B ) TYPE: amino acid  
( D ) TOPOLOGY: linear

( i i ) MOLECULE TYPE: protein

( x i ) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

Met	Ala	Arg	Lys	Asp	Val	Ala	Ser	Met	Phe	Ala	Val	Ala	Leu	Phe	Ile	
- 28			- 25					- 20					- 15			
Gly	Ala	Phe	Ala	Ala	Val	Pro	Thr	Ser	Val	Gln	Ser	Ile	Gly	Val	Cys	
		- 10					- 5					1				
Tyr	Gly	Val	Ile	Gly	Asn	Asn	Leu	Pro	Ser	Arg	Ser	Asp	Val	Val	Gln	
5					10					15					20	
Leu	Tyr	Arg	Ser	Lys	Gly	Ile	Asn	Gly	Met	Arg	Ile	Tyr	Phe	Ala	Asp	
				25					30					35		
Gly	Gln	Ala	Leu	Ser	Ala	Val	Arg	Asn	Ser	Gly	Ile	Gly	Leu	Ile	Leu	
			40					45					50			
Asp	Ile	Gly	Asn	Asp	Gln	Leu	Ala	Asn	Ile	Ala	Ala	Ser	Thr	Ser	Asn	
		55					60					65				
Ala	Ala	Ser	Trp	Val	Gln	Asn	Asn	Val	Arg	Pro	Tyr	Tyr	Pro	Ala	Val	
	70					75					80					

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

(A) NAME: Logemann, Juergen  
(B) STREET: Lavendeltuyn 5  
(C) CITY: NB Leiden  
(E) COUNTRY: The Netherlands  
(F) POSTAL CODE (ZIP): 2317

(A) NAME: Jach, Guido  
(B) STREET: Maternusstrasse 22  
(C) CITY: Koeln  
(E) COUNTRY: Germany  
(F) POSTAL CODE (ZIP): 50678

(A) NAME: Goernhardt, Birgit  
(B) STREET: Auf dem Knoepp 28  
(C) CITY: Koeln  
(E) COUNTRY: Germany  
(F) POSTAL CODE (ZIP): 51145

(A) NAME: Mundy, John  
(B) STREET: NY Carlsberg Vej 6, 4th  
(C) CITY: V Copenhagen  
(E) COUNTRY: Denmark  
(F) POSTAL CODE (ZIP): 1760

(A) NAME: Schell, Jeff  
(B) STREET: Carl-von-Linne-Weg 10  
(C) CITY: Koeln  
(E) COUNTRY: Germany  
(F) POSTAL CODE (ZIP): 50829

(A) NAME: Eckes, Peter  
(B) STREET: Am Flachslund 18  
(C) CITY: Kelkheim (Taunus)  
(E) COUNTRY: Germany  
(F) POSTAL CODE (ZIP): 65779

(A) NAME: Chet, Ilan  
(B) STREET: Shikun Ezrachi  
(C) CITY: Nes Ziona  
(E) COUNTRY: Israel  
(F) POSTAL CODE (ZIP): 70400

(ii) TITLE OF INVENTION: Transgenic pathogen-resistant organism

(iii) NUMBER OF SEQUENCES: 12

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Baker & Botts  
(B) STREET: 30 Rockefeller Plaza  
(C) CITY: New York  
(D) STATE: New York  
(E) COUNTRY: U.S.A.  
(F) ZIP: 10112

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: reissue application of U.S. Patent No. 5,804,184  
(B) FILING DATE: herewith

(vii) ATTORNEY/AGENT INFORMATION:

(A) ATTORNEY NAME: Tenser, Arthur  
(B) REGISTRATION NUMBER: 18,839  
(C) AGENT NAME: Kole, Lisa  
(D) REGISTRATION NUMBER: 35,225  
(E) REFERENCE NO: A29542 FWC I- 37/31335

(viii) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (212) 408-2500  
(B) TELEFAX: (212) 765-2519  
(C) TELEX: 238555

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 275 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Aspergillus giganteus*

(ix) FEATURE:

(A) NAME/KEY: 5'UTR  
(B) LOCATION: 1..45

(ix) FEATURE:

(A) NAME/KEY: CDS  
(B) LOCATION: 46..225  
(C) IDENTIFICATION METHOD: experimental  
(D) OTHER INFORMATION: /codon\_start= 46  
/function= "antifungal agent"

/product= "antifungal peptide) "  
 /evidence= EXPERIMENTAL  
 /note= "antifungal agent, especially on  
 Rhizoctonia solani, various Aspergillus, Fusaria  
 and Trichophyton species"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

TTGCCACCCC CGTTGAAGCC GATTCTCTCA CCGCTGGTGG TCTGG ATG CAA GAG	54
Met Gln Glu	
1	
ATG AGA GCG CGG GTT TTG GCC ACA TAC AAT GGC AAA TGC TAC AAG AAG	102
Met Arg Ala Arg Val Leu Ala Thr Tyr Asn Gly Lys Cys Tyr Lys Lys	
5 10 15	
GAT AAT ATC TGC AAG TAC AAG GCA CAG AGC GGC AAG ACT GCC ATT TGC	150
Asp Asn Ile Cys Lys Tyr Lys Ala Gln Ser Gly Lys Thr Ala Ile Cys	
20 25 30 35	
AAG TGC TAT GTC AAA AAG TGC CCC CGC GAC GGC GCG AAA TGC GAG TTT	198
Lys Cys Tyr Val Lys Lys Cys Pro Arg Asp Gly Ala Lys Cys Glu Phe	
40 45 50	
GAC AGC TAC AAG GGG AAG TGC TAC TGC TAGACGGTGA GCGAAGGGAC	245
Asp Ser Tyr Lys Gly Lys Cys Tyr Cys	
55 60	
GAAGTAGGCT GGGGGTTATT TTACTCTGCT	275

(3) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met Gln Glu Met Arg Ala Arg Val Leu Ala Thr Tyr Asn Gly Lys Cys	
1 5 10 15	
Tyr Lys Lys Asp Asn Ile Cys Lys Tyr Lys Ala Gln Ser Gly Lys Thr	
20 25 30	
Ala Ile Cys Lys Cys Tyr Val Lys Lys Cys Pro Arg Asp Gly Ala Lys	

45

Cys Glu Phe Asp Ser Tyr Lys Gly Lys Cys Tyr Cys  
50 55 60

(4) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: C-terminal

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Aspergillus giganteus*

(ix) FEATURE:

- ```
(A) NAME/KEY: Protein
(B) LOCATION: 1..51
(D) OTHER INFORMATION: /note= "active protein fragment of
AFP"
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

Ala Thr Tyr Asn Gly Lys Cys Tyr Lys Lys Asp Asn Ile Cys Lys Tyr  
1 5 10 15

Lys Ala Gln Ser Gly Lys Thr Ala Ile Cys Lys Cys Tyr Val Lys Lys  
20 25 30

Cys Pro Arg Asp Gly Ala Lys Cys Glu Phe Asp Ser Tyr Lys Gly Lys  
35 40 45

Cys Tyr Cys  
50

(5) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1032 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA



(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Hordeum vulgare
- (B) STRAIN: L.cv. Piggy

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA gene bank in lambda-gt-11-phages

(ix) FEATURE:

- (A) NAME/KEY: 5'UTR
- (B) LOCATION: 1..42

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 43..885
- (D) OTHER INFORMATION: /codon\_start= 43  
/function= "antifungal activity"  
/product= "protein synthesis inhibitor (PSI)"  
/note= "antifungal activity, especially on spores  
of Trichoderma reesii and Fusarium sporotrichoides  
and on Rhizoctonia solani."

(ix) FEATURE:

- (A) NAME/KEY: 3'UTR
- (B) LOCATION: 886..1032
- (D) OTHER INFORMATION: /partial  
/note= "46 nucleotides at the 3'-end not shown."

(ix) FEATURE:

- (A) NAME/KEY: polyA\_signal
- (B) LOCATION: 930..935
- (D) OTHER INFORMATION: /note= "potential polyadenylation  
signal"

(ix) FEATURE:

- (A) NAME/KEY: polyA\_signal
- (B) LOCATION: 963..976
- (D) OTHER INFORMATION: /note= "potential polyadenylation  
signal"

(ix) FEATURE:

- (A) NAME/KEY: polyA\_signal
- (B) LOCATION: 1002..1011
- (D) OTHER INFORMATION: /note= "potential polyadenylation  
signal"

(ix) FEATURE:

- (A) NAME/KEY: mat\_peptide
- (B) LOCATION: 46..886

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

CTTAATAGCA CATCTTGTCC GTCTTAGCTT TGCATTACAT CC ATG GCG GCA AAG